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Cooperation of TaCKX genes in regulation of growth and productivity of wheat (*Triticum aestivum* L.)

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Multigene family of CKX genes encoding cytokinin oxidase / dehydrogenase (CKX) enzymes, affect cytokinin-regulated processes including plant growth and plant productivity. Their expression in different plants is tissue and developmentally specific. The detailed biological function of most of the TaCKX genes in wheat is not known. The goal of this research is to select those, which correlate with yield-related traits in wheat breeding material. In our earlier research we showed that expression level of HvCKX genes in developing kernels and seedling roots of barley may indicated their role in growth and productivity (Zalewski et al. 2010, 2014). Therefore the first step of current project was to analyze specificity of expression of all 11 TaCKX family genes in developing plants of wheat and their cooperation within and among organs (Ogonowska et al. 2019). Based on these and other our research on the role of TaCKX genes in determining yield-related traits, we have been chosen the most important ones to test breeding material of wheat (30 breeding lines and cultivars, selected F1 and segregating progeny). There were: TaCKX1, TaCKX2.1, TaCKX2.2 and TaCKX3 for 7-14 DAP (days after pollination) spike development, and TaCKX1, TaCKX5 and TaCKX6 for seedling root development. Correlation coefficients between expression levels of TaCKX genes and activity of CKX enzymes with phenotypic traits were calculated. In 7 DAP spikes expression level of TaCKX1 strongly and positively correlated with expression level of TaCKX3 and in seedling roots with TaCKX5 and TaCKX6. Moreover expression of TaCKX1 significantly and positively correlated with the mass of seedling roots and thousand grain weight (TGW), and expression of TaCKX6 with the productivity. Negative, significant correlation was also observed between levels of expression of some TaCKX genes in developing kernels and selected phenotypic traits. The possible mechanism of cooperation of TaCKX genes in regulation of growth and productivity of common wheat will be discussed.

Recent Publications

1. Ogonowska H, Barchacka K, Gasparis S, Jablonski B, Orczyk W, Dmochowska-Boguta M, Nadolska-Orczyk A (2019) Specificity of Expression of TaCKX Family Genes in Developing Plants of Wheat and Their Co-Operation Within and Among Organs. PLOS ONE 14 (4):e0214239.
2. Gasparis S., Kała M., Przyborowski M., Łyżnik L., Orczyk W., Anna Nadolska-Orczyk. 2018. A simple and efficient CRISPR/Cas9 platform for induction of single and multiple, heritable mutations in barley (*Hordeum vulgare* L.). Plant Methods, 4:111.
3. Nadolska-Orczyk A, Rajchel IK, Orczyk W, Gasparis S. 2017. Major genes determining yield-related traits in wheat and barley. Theor. Appl. Genet., 130:1081–1098, DOI: 10.1007/s00122-017-2880-x.
4. Zalewski W., Gasparis S., Boczkowska M., Rajchel I.K., Kała M., Orczyk W., Nadolska-Orczyk A. 2014. Expression patterns of HvCKX genes indicate their role in growth and reproductive development of barley. PLoS ONE 9(12):1-20: e115729.
5. Zalewski W., Galuszka P., Gasparis S., Orczyk W., Nadolska-Orczyk A. 2010. Silencing of the HvCKX1 gene decreases the cytokinin oxidase/dehydrogenase level in barley and leads to higher plant productivity. J. Exp. Bot. 61 (6): 1839-1851.

Biography

Anna Nadolska-Orczyk is a Full technology to functional genomics wheat development and productivity technology to analyze gene function

Notes: